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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jofuku, K. Diane
Okamuro, Jack K.
- (ii) TITLE OF INVENTION: Methods for Improving Seeds
- (iii) NUMBER OF SEQUENCES: 99
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/879,827
(B) FILING DATE: 20-JUN-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/700,152
(B) FILING DATE: 20-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Bastian, Kevin L.
(B) REGISTRATION NUMBER: 34,774
(C) REFERENCE/DOCKET NUMBER: 023070-067210US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 576-0200
(B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1669
(D) OTHER INFORMATION: /note= "canola APETALA2 (AP2) domain containing (ADC) gene"
- (ix) FEATURE:
(A) NAME/KEY: misc feature
(B) LOCATION: 1..592
(D) OTHER INFORMATION: /note= "gene sequences 5' to start site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCNGNGTT TTCCNTNATN GTTCGTGGCG GCCCACGTGG TAGGAGAAGA CGGAAATTAA 60
 CAAATTCATN GTCACCCTAC AAGAAAGGGG GAACATAATT AAATTTTCGAG TAGTTGGAGT 120
 AGGAGAAGCT CAATAGTACA AGAAATTAAA TAAGATACTC CCATCTACAT CATCTTGCTT 180
 TTTCTCATCC CATAATAGTT TTCCAGTAAA ACTGTGAACC TTGTGAATTT AATTTCCCTT 240
 TTATATATAA AGATACCTTG TGGTGTTTAT ACTCAGGAGA CCAGAAACTA GGAAACAGTC 300
 TATTACATTT GTATTGGGAA ATAATCAAAT CTCAAAATTT GATTCATTCA TAAACTTTAT 360
 ACTATATACT TTTTCGTTGA TAAATTTTTT GCCTCTCCTT CTAATAACGA ATGGAGTCCT 420
 AGCACATATA TATTNCCTAA TGTGATTTTC ATTTTCATATG GATATTTATT TATATATGAC 480
 TATTTATTCC ATCCCATCTT ATTGCTTTTG ATGGTTCTCT TGTCATTAGA GTCTTCTCTC 540
 TTATTGCTCT CATATTTCTT TGCTTTTGTT TCCTCTTTAT TACAAGAGAG ATATGTGGAA 600
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 TGTACCAATC TCTATGAGAT CATCGACCAC GTGTCTGTCG TCTGTTCCCTC CCGTGACCCG 720
 GATATTTTTT TCCGAATCAA ATCATGGAAC AGGAAGTTCC AGGAATATCT GGGTCCCGTA 780
 TCACTAGAAA CCAGTCTCTT GTTCGGTCGA ATCCTAGCGG GTCTGGTCGT CCGGAAAACC 840
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 CTCAGTATAG AGGAGTTACT TTTTATCGAC GAACCCGAAG ATGGGAGTCA CATATTTGGT 960
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 ATCAAATACA TGTTTCATTT CATTTGAGCC NATACCGTAT TGTTGTTTTT AAAATATGTT 1080
 TGGAATCTTA TGCAGGGACT GCGGGAAGCA AGTGTACTTA GGTATGATCA TGTAATGTTG 1140
 TTCAAACACA GATCAAATAT CCTATTGAAA CTAAGTTGTG TTGTGTCTGT CCATTTTTAT 1200
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 TCAATTAGAA CGAATCTAAT ATTCCTTATT TTGTAATTTG CTGATATACA AATTAATTTG 1380
 GGTGGGTAAC TGTTTGGGAC AGTGCCTACG ATAGAGCCGC AGTTAAGTTT AGAGGTGTAG 1440
 ATGCAGATAT AAATTTCAAT ATTGAAGACT ATGTGGAGGA TTTGAAACAG GTAAAATATT 1500
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 ATTTGTTGCA GATGACGCAG TTGACAAAGG AAGAGTTCAT GCATGTCATT AGAAGGCAAA 1620
 GCACTGGGTT TCCAAGAGGC AGCTCTAAGT ATAGAGGTGT CACTTTGCA 1669

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..803
- (D) OTHER INFORMATION: /note= "soybean APETALA2 (AP2) gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATTGTGGG AAACAAGTTT ATCTAGGTAA AGTTGATTAA TAACAATAAT TGTATATGTG 60
 TTTGTGAGAA CTGTGGCAGT TATTTTTCCT AATATTGTTT TAAGAGGCTA AAACGGTTTT 120
 TTTTTCCTTG TTTTGTGTTT TTTGTCTTGG CTGTGATGCG GTAGAGACAA GAGTGTGAGT 180
 GTGTGTTGTG TGTGGGTGAG GATTTTTTTR TTTTTTGTG GTGACTGACT TGATGGTTTT 240
 TGTCTGGGTA AAATTTGTCT AGGTGGATTT GACACAGCAC ATGCCGCTGC TCGGTGAGCC 300
 CTTGCCCCCT CCTTTAGTAT TATACCAAGC TTGTAATATT ACTTTTTCCA TGTCTTGAAC 360
 CAAATATCAA ATATTATTGT AAATCACATT TCGTTGTGGG CCGGGGAATT GTGAGTCTCA 420
 AAGAAAATTG TGTATTTTCC GTCTCTCTTT TCAGTGCTTA TGATAGAGCG GCTATTAAAT 480
 TCCGAGGAGT GGAGGCTGAC ATTAACCTCA ATATTGGAGA CTATGAAGAT GACTTGAAGC 540
 AGGTGATCAA TTTGTGGATT ATGTTTTTTT TATTCGATAT AAATGCATTT ATCGTATTTA 600
 TCTTATCTTG AACAGTCATA CGTATAGGAT GCACCTTATC TCCTACAGTT AGTGTTTTTT 660
 TTTATCTTGA ATTATTCTCA TGATTTTGTT AAATGCAATG TTAATAGATG AGCAATCTTA 720
 CCAAGGAAGA GTTCGTCCAC GTGCTTCGCC GCCAAAGCAC TGGATTTCGG AGAGGAAGCT 780
 CCAAGTATAG AGGTGTCACT TGC 803

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..11721
- (D) OTHER INFORMATION: /note= "Arabidopsis APETALA2 (AP2) genomic sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTAAGCAATA ATATAGTTTG AACAATGAGT TCAAAAGCCT TTGGTTGGAA TAACTCATTA 60
 AGAAAACAGA TAGTTTAAAA TCAATTGAAT TATGATTTC A GACATAGTAT AAGTTTGGGC 120
 AAAGTATTTT AATGGAAATA GAATACAAAC TTGATAACAA GTTATTGCCA TTTAGAAAAT 180
 GTTATAACTC CTTATATAGT GAGAACCCTA TTGCTTGCTT GTGTTCAAGG AATTGCTGTT 240

TATGGAAGCTC CACTTTAAAT AAACATATAA ATAATCTATT TAGTATCAAA AACTTAATAT 300
 CCCATCTACT TTGAATTTGC CCGATCATGA AAACACCTAT TTATTGTACA TAAATATACA 360
 TCTTTAACAA ATATAGATCT ATTTGTATTT GTATCTTATT ACCTTTTATT CATATAGAAA 420
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 ATTGTGGGGT TTTGAAGTAA TCTACTAGAT TATTCATTTT CTTGCAAAAA ACACCTTTTT 540
 ATAGTTGCTT ACCGAACCAA GCCGTGGACT TCACTTTCTT AAAACATGAA ATTACATATT 600
 AAAGGAATCT TTTGATTAAT CAAAGAAGAT GTTTGTATAC ATAGATAATA AATGAAAGTG 660
 GAAATATTTT TTTTAAAT AAAGAAAAA AATAAAGAAA CTCCAATACG AGGAATTGTT 720
 TCGAATATAA TCTTTTTTCC AAAGAAAGCA AGTGGTTAGA GAGAGAATAA TATTATTTTA 780
 TTAAATTTTT ACAAAAAAA CAGTGACAAG AGAAGAGAGA GAGAGAAAGG GCAGTGGAAG 840
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 TTTTATTTT TCTCTCTCT CTCTTTAGCT CTTTTTTTTT TGTTTTTATT AAAGTTTTTA 960
 TTTTATTTT TACCAACCAA AAGCTTTTCT CTTTGGTTTC TCTTATTTAG CTTCTAACCT 1020
 TGAGGAGAAT CATACCAGAG GATTGAAGTT TGAACCTTCA AAGATCAAAA TCAAGAAACC 1080
 AAAAAAAAC AAAAAAATG TGGGATCTAA ACGACGCACC ACACCAAACA CAAAGAGAAG 1140
 AAGAATCTGA AGAGTTTTGT TATTCTTCAC CAAGTAAACG GGTGGATCT TTCTCTAATT 1200
 CTAGCTCTTC AGCTGTTGTT ATCGAAGATG GATCCGATGA CGATGAACTT AACCGGGTCA 1260
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 CTCATCAAAA TTGGCTGCAG ACAAATGGCT TCCAACCTCC TCTCATGAGA CCTTCTTGAA 3240
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 TTGAGATGTT CTGACTAAAA AGGTTGAGAA GAGATTTGTC AATGAGTTGT CTTTTGTTGT 3540
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 AGAAAGGAAG TGAAGCCGAG AAGTCTCTCT CACCATTATA ACAATGTCTG ACTTCTTTTG 6480
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 ATAATGAAAA TCAATTAGTA ACGAGAAAAA CACATTATAC AACAATGTGT GTTGTAGAAT 9360
 CAAACAAAAA GACATTTACC TAGCAGCTTC GACCTCGGTG TCGAACAAAC CCAAATAAAC 9420
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 ACCAATATAG TTTATAATTT ATATTTACCT GTTCAAGTC ATCATCATAA TCTTCGATGT 9780
 TGAAATTGAT ATCCGCTTCT ACTCCACGGA ATTTAATAGC AGCTCTATCA TATGCTCTAT 9840
 TAAATAAAAC AAAATTAAAA TTAATTTTAA TAAATTTCTT CCGGTATTTT TAAAAAATA 9900
 AATAAATAAC AACTCAATAT AGAGAGAGTC AAAGAGAGAA AAATACCGAG CTGCTGCATG 9960
 AGCAGTGTCA AATCCACCTA TTCAGAGNTT ATAATAAAAT AAAATTATGA TGACATTTTT 10020
 CAACACCAAA ATACAAAAAA AAACATGAGG AAAATAAAAT TACCTAAGTA AACTTGTTTC 10080
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 CGGTACGCCG GTAAAACGTA ACACCTCTAT ACTGAGAACT TCTTGATCTT GGTCCACGCC 10260
 GACTCTTTTT CAACGGCTGT GCCGGCTCCA CTACGGCAGC GGCAACGTTG GTAGCTTTAC 10320
 CCGCGGACGA TCCGGTGGCT AGATCCGACT GACAAAACTT AACACCAAAC CAGTGAGCCC 10380
 GAGGAAAGCC AGAAGCAACA CCACCGCCGT TAGAATCCAT CTCAGGGAAG AACTGATGGG 10440

TGACAAGTGG GTTATTGGGT CTGACCCGGT TAAGTTCATC GTCATCGGAT CCATCTTCGA 10500
 TAACAACAGC TGAAGAGCTA GAATTAGAGA AAGATCCAAC CCGTTTACTT GGTGAAGAAT 10560
 AACAAAACCTC TTCAGATTCT TCTTCTCTTT GTGTTTGGTG TGGTGCGTCG TTTAGATCCC 10620
 ACATTTTTTTT TGTTTTTTTTT TGGTTTCTTG ATTTTGATCT TTGAAGGTTT AACTTCAAT 10680
 CCTCTGGTAT GATTCTCCTC AAGGTTAGAA GCTAAATAAG AGAAACCAA GAGAAAAGCT 10740
 TTTGGTTGGT AGAAAATAAA ATAAAAACTT TAATGAAAAC AAAAAAAAAA GAGCTAAAGA 10800
 GAGAGAGAGA AGAAAATAAA ATAAAAATTT GATAGATTGC TTCTACGAAA GCTTTCATTT 10860
 TTATCCTTTC CTTTATATTT ACTTCCACTG CCCTTCTCTCT CTCTCTCTTC TCTTGCTACT 10920
 GTTTTTTTTG TAAAAATTTA ATAAAAATAAT ATTATTCTCT CTCTAACCAC TTGCTTCTT 10980
 TGGAAAAAAG ATTATATTCG AAACAATTCC TCGTATTGGA GTTCTTTTAT TTTTTTCTT 11040
 TATTTTAAAA AAAAATATTT CCACTTTCAT TTATTATCTA TGTATACAAA CATCTTCTTT 11100
 GATTAATCAA AAGATTCCTT TAATATGTAA TTTTATGTTT TAAGAAAGTG AAGTCCACGG 11160
 CTTGGTTCGG TAAGCAACTA TAAAAAGGTG TTTTTTGCAA GAAAATGAAT AATCTAGTAG 11220
 ATTACTTCAA AACCCACAA TACTGCCAAT TTTGATATAC TTTAACTCT TGGAACAAAG 11280
 CTTTTTGTTT GTTTTTTCCT TTTTCTATAT GAATAAAAGG TAATAAGATA CAAATACAAA 11340
 TAGATCTATA TTTGTTAAAG ATGTATATTT ATGTACAATA AATAGGTGTT TTCATGATCG 11400
 GGCAAATTCA AAGTAGATGG GATATTAAGT TTTTGATACT AAATAGATTA TTTATATGTT 11460
 TATTTAAAGT GGAGTTCCAT AAACAGCAAT TCCTTGAACA CAAGCAAGCA ATAGGGTTCT 11520
 CACTATATAA GGAGTTATAA CATTTTCTAA ATGGCAATAA CTTGTTATCA AGTTTGTATT 11580
 CTATTTCCAT TAAATACTT TGCCCAAAC TATACTATGT CTGAAATCAT AATTCAATTG 11640
 ATTTTAAACT ATCTGTTTTT TTAATGAGTT ATTCCAACCA AAGGCTTTTG AACTCATTGT 11700
 TCAAACTATA TTATTGCTTA C 11721

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: /note= "AP2-R1 direct repeat at positions 129 to 195"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 32..49
- (D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic alpha-helix (SEQ ID NO:6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
 1 5 10 15
 Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
 20 25 30
 Thr Asp Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
 35 40 45
 Phe Arg Gly Val Glu Ala Asp Ile Asn Phe Asn Ile Asp Asp Tyr Asp
 50 55 60
 Asp Asp Leu
 65

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..68
 (D) OTHER INFORMATION: /note= "AP2-R2 direct repeat at
 positions 221 to 288"

(ix) FEATURE:

- (A) NAME/KEY: Region
 (B) LOCATION: 33..50
 (D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic
 alpha-helix (SEQ ID NO:7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu
 1 5 10 15
 Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Tyr Val Tyr Leu Gly Leu
 20 25 30
 Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile
 35 40 45
 Lys Cys Asn Gly Lys Asp Ala Val Thr Asn Phe Asp Pro Ser Ile Tyr
 50 55 60
 Asp Glu Glu Leu
 65

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..18

(D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic
alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Phe Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile
1 5 10 15

Lys Phe

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..18

(D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic
alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile
1 5 10 15

Lys Cys

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Ala Tyr Asp

1

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: /note= "ANT-R1 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 44..59
- (D) OTHER INFORMATION: /note= "putative ANT-R1 amphipathic alpha-helix (SEQ ID NO:37)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Ser Gln Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr
 1 5 10 15
 Glu Ala His Leu Trp Asp Asn Ser Phe Lys Lys Glu Gly His Ser Arg
 20 25 30
 Lys Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Met Glu Glu Lys Ala
 35 40 45
 Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Ser Thr
 50 55 60
 His Thr Asn Phe Ser Ala Glu Asn Tyr Gln Lys Glu Ile
 65 70 75

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "ANT-R2 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 37..51
- (D) OTHER INFORMATION: /note= "putative ANT-R2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ser Ile Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp
 1 5 10 15
 Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly
 20 25 30
 Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala
 35 40 45
 Ile Lys Phe Arg Gly Thr Asn Ala Val Thr Asn Phe Asp Ile Thr Arg
 50 55 60
 Tyr Asp Val Asp Arg
 65

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: /note= "RAP2.7-R1 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 33..49
- (D) OTHER INFORMATION: /note= "putative RAP2.7-R1 amphipathic alpha helix (SEQ ID NO:36)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
 1 5 10 15
 Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
 20 25 30
 Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
 35 40 45
 Phe Arg Gly Val Asp Ala Asp Ile Asn Phe Thr Leu Gly Asp Tyr Glu
 50 55 60
 Glu Asp Met
 65

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: /note= "RAP2.7-R2 direct repeat"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 26..34
- (D) OTHER INFORMATION: /note= "putative RAP2.7-R2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu
1      5      10      15
Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Ala Tyr Asp Lys Ala Ala
      20      25      30
Ile Asn Thr Asn Gly Arg Glu Ala Val Thr Asn Phe Glu Met Ser Ser
      35      40      45
Tyr Gln Asn Glu Ile
      50

```

(2) INFORMATION FOR SEQ ID NO:13:

- ad*
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Tyr Arg Gly Val Thr
1      5

```

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ala or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Arg Trp Glu Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Tyr Leu Gly
1

(2) INFORMATION FOR SEQ ID NO:16:

- Q4
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Ala Ile Lys
1

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco
EREBP-1"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..51
- (D) OTHER INFORMATION: /note= "putative EREBP-1 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Gly Arg His Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala
1           5           10           15
Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
20           25           30
Thr Tyr Glu Thr Asp Glu Glu Ala Ala Ile Ala Tyr Asp Lys Ala Ala
35           40           45
Tyr Arg Met Arg Gly Ser Lys Ala His Leu Asn Phe Pro Leu Glu Val
50           55           60
Ala Asn Phe Lys Gln
65

```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-2"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..51
- (D) OTHER INFORMATION: /note= "putative EREBP-2 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Gly Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
1           5           10           15
Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly
20           25           30
Thr Tyr Glu Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys Ala Ala
35           40           45
Tyr Arg Met Arg Gly Ser Lys Ala Leu Leu Asn Phe Pro His Arg Ile
50           55           60
Gly Leu Asn Glu Pro
65

```


(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-3"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative EREBP-3 amphipathic alpha-helix (SEQ ID NO:41)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu Val His Tyr Arg Gly Val Arg Lys Arg Pro Trp Gly Arg Tyr Ala
 1 5 10 15
 Ala Glu Ile Arg Asp Pro Gly Lys Lys Ser Arg Val Trp Leu Gly Thr
 20 25 30
 Phe Asp Thr Ala Glu Glu Ala Ala Lys Ala Tyr Asp Thr Ala Ala Arg
 35 40 45
 Glu Phe Arg Gly Pro Lys Ala Lys Thr Asn Phe Pro Ser Pro Thr Glu
 50 55 60
 Asn Gln Ser Pro
 65

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: /note= "AP2 domain within tobacco EREBP-4"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..51
- (D) OTHER INFORMATION: /note= "putative EREBP-4 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
 1 5 10 15
 Ala Glu Ile Arg Asp Pro Asn Arg Lys Gly Thr Arg Val Trp Leu Gly
 20 25 30
 Thr Phe Asp Thr Ala Ile Glu Ala Ala Lys Ala Tyr Asp Arg Ala Ala
 35 40 45
 Phe Lys Leu Arg Gly Ser Lys Ala Ile Val Asn Phe Pro His Arg Ile
 50 55 60
 Gly Leu Asn Glu Pro
 65

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.2 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..51
- (D) OTHER INFORMATION: /note= "putative RAP2.2 amphipathic alpha-helix (SEQ ID NO:38)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala
 1 5 10 15
 Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr
 20 25 30
 Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg
 35 40 45
 Arg Ile Arg Gly Thr Lys Ala Lys Val Asn Phe Pro Glu Glu Lys Asn
 50 55 60
 Pro Ser Val Val
 65

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.3 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..50
- (D) OTHER INFORMATION: /note= "putative RAP2.3 amphipathic alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Lys Asn Val Tyr Arg Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala
1           5           10           15
Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr
                20           25           30
Phe Asn Thr Ala Glu Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys
                35           40           45
Gln Ile Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Asp Leu His His
50           55           60
Pro Pro Pro Pro
65

```

ay (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.5 AP2 domain"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.5 amphipathic alpha-helix (SEQ ID NO:39)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Glu Ile Arg Tyr Arg Gly Val Arg Lys Arg Pro Trp Gly Arg Tyr Ala
1           5           10           15
Ala Glu Ile Arg Asp Pro Gly Lys Lys Thr Arg Val Trp Leu Gly Thr
                20           25           30

```

Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Thr Ala Ala Arg
35 40 45

Asp Phe Arg Gly Ala Lys Ala Lys Thr Asn Phe Pro Thr Phe Leu Glu
50 55 60

Leu Ser Asp Gln
65

(2) INFORMATION FOR SEQ ID NO:24:

- ```

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear,

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..68
 (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis
 RAP2.6 AP2 domain"

(ix) FEATURE:
 (A) NAME/KEY: Region
 (B) LOCATION: 34..51
 (D) OTHER INFORMATION: /note= "putative RAP2.6 amphipathic
 alpha-helix"

```

54

[illegible]

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

```

 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..68
 (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis
 RAP2.12 AP2 domain"

```

```

 (A) NAME/KEY: Region
 (B) LOCATION: 34..51
 (D) OTHER INFORMATION: /note= "putative RAP2.12 amphipathic
 alpha-helix (SEQ ID NO:40)"

```

Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala  
1 5 10 15

Ala Glu Ile Arg Asp Pro Arg Glu Gly Ala Arg Ile Trp Leu Gly Thr  
20 25 30

Phe Lys Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg  
35 40 45

Arg Ile Arg Gly Ser Lys Ala Lys Val Asn Phe Pro Glu Glu Asn Met  
50 55 60

Lys Ala Asn Ser  
65

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 68 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..68  
(D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis TINY  
AP2 domain"

(A) NAME/KEY: Region  
(B) LOCATION: 35..50  
(D) OTHER INFORMATION: /note= "putative TINY amphipathic  
alpha-helix"

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Val | Tyr | Arg | Gly | Val | Arg | Lys | Arg | Asn | Trp | Gly | Lys | Trp | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Glu | Ile | Arg | Glu | Pro | Arg | Lys | Lys | Ser | Arg | Ile | Trp | Leu | Gly | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Phe | Pro | Ser | Pro | Glu | Met | Ala | Ala | Arg | Ala | His | Asp | Val | Ala | Ala | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Ser Ile Lys Gly Ala Ser Ala Ile Leu Asn Phe Pro Asp Leu Ala Gly  
 50 55 60

Ser Phe Pro Arg  
 65

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..68  
 (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis  
 RAP2.1 AP2 domain"

- (ix) FEATURE:  
 (A) NAME/KEY: Region  
 (B) LOCATION: 35..50  
 (D) OTHER INFORMATION: /note= "putative RAP2.1 amphipathic  
 alpha-helix"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg Lys Pro Tyr Arg Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val  
 1 5 10 15

Ala Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser  
 20 25 30

Tyr Thr Thr Asp Ile Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe  
 35 40 45

Tyr Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu  
 50 55 60

Gln Glu Glu Asp  
 65

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..68  
 (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis  
 RAP2.4 AP2 domain"

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 35..50
- (D) OTHER INFORMATION: /note= "putative RAP2.4 amphipathic alpha-helix"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Thr Lys Leu Tyr Arg Gly Val Arg Gln Arg His Trp Gly Lys Trp Val
1 5 10 15
Ala Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu Trp Leu Gly Thr
20 25 30
Phe Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys Ala Ala Tyr
35 40 45
Lys Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro Asn Leu Arg His
50 55 60
Asn Gly Phe His
65

```

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.8 AP2 domain"

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 33..48
- (D) OTHER INFORMATION: /note= "putative RAP2.8 amphipathic alpha-helix"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ab

```

Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly
1 5 10 15
Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn
20 25 30
Glu Gln Glu Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys Arg Phe
35 40 45
Arg Gly Arg Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu Asp Gly
50 55 60
Asp Leu
65

```

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.10 AP2 domain"

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 36..51
- (D) OTHER INFORMATION: /note= "putative RAP2.10 amphipathic alpha-helix"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp Lys Pro Tyr Lys Gly Ile Arg Met Arg Lys Trp Gly Lys Trp Val  
 1                      5                      10                      15  
 Ala Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Ile Trp Leu Gly Ser  
                     20                      25                      30  
 Tyr Ser Thr Pro Glu Ala Ala Ala Arg Ala Tyr Asp Thr Ala Val Phe  
                     35                      40                      45  
 Tyr Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Glu Leu Leu Ala  
 50                      55                      60  
 Gly Val Thr Val  
 65

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: /note= "EREBP-like Arabidopsis RAP2.11 AP2 domain"

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 34..50
- (D) OTHER INFORMATION: /note= "putative RAP2.11 amphipathic alpha-helix"



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Lys Thr Lys Phe Val Gly Val Arg Gln Arg Pro Ser Gly Lys Trp Val  
 1                      5                      10                      15  
 Ala Glu Ile Lys Asp Thr Thr Gln Lys Ile Arg Met Trp Leu Gly Thr  
                     20                      25                      30  
 Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu Ala Ala Cys  
                     35                      40                      45  
 Leu Leu Arg Gly Ser Asn Thr Arg Thr Asn Phe Ala Asn His Phe Pro  
                     50                      55                      60  
 Asn Asn Ser Gln  
 65

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Val or Ile"

 a4  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Tyr Arg Gly Xaa Arg  
 1                      5

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = positively charged  
amino acid"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Trp, Phe or Tyr"

```
(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Asp or Glu"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Trp Gly Xaa Xaa Xaa Ala Glu Ile Xaa Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Ser or Thr"
```

```
(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = Tyr or Phe"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Trp Leu Gly Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Ile, Leu or positively  
charged amino acid"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Glu Ala Ala Xaa Ala Tyr Asp  
1 5

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "putative RAP2.7-R1 amphipathic  
alpha-helix"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asp Thr Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys  
1 5 10 15  
Phe

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative ANT-R1 amphipathic  
alpha-helix"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative RAP2.2 amphipathic alpha-helix"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg  
 1                      5                      10                      15  
 Ile Arg

## (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

68 (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative RAP2.5 amphipathic alpha-helix"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Thr Ala Ala Arg Asp Phe  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "putative RAP2.12 amphipathic alpha-helix"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg  
 1                      5                      10                      15  
 Ile Arg

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "putative EREBP-3 amphipathic alpha-helix"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Thr Ala Glu Glu Ala Ala Lys Ala Tyr Asp Thr Ala Ala Arg Glu Phe  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "AP2 linker region"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Lys Gln Met Thr Asn Leu Thr Lys Glu Glu Phe Val His Val Leu Arg  
 1                      5                      10                      15  
 Arg Gln Ser Thr Gly Phe Pro Arg Gly  
                     20                      25

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "ANT linker region"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Glu Asp Met Met Lys Asn Met Thr Arg Gln Glu Tyr Val Ala His Leu  
 1 5 10 15  
 Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly  
 20 25

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "RAP2.7 linker region"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

*as*  
 Met Lys Gln Val Gln Asn Leu Ser Lys Glu Glu Phe Val His Ile Leu  
 1 5 10 15  
 Arg Arg Gln Ser Thr Gly Phe Ser Arg Gly  
 20 25

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = positively charged amino acid"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Asn Leu Thr Xaa Glu Glu Phe Val His  
 1 5

## (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu Arg Arg Gln Ser Thr Gly Phe Ser Arg Gly  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JOAP2U primer"

GF (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTTGCCGCTG CCGTAGTG

18

## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JOAP2L primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGTTCATCCT GAGCCGCATA TC

22

## (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "JORAP2.1U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTCAAGAAGA AGTGCCTAAC CACG

24

## (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.1L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAGAAGCTA GAAGAGCGTC GA

22

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JORAP2.2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAAAATGGG CTGCGGAG

18



## (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.2L primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTTACCTCCA GCATCGAACG AG

22

## (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.4U primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCTGGATCTT GTTTCGCTTA CG

22

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.4L primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCTTCAAGCT TAGCGTCGAC TG

22

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "JORAP2.5U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGATGGGCTT GAAACCCGAC

20

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "JORAP2.5L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTGGCTAGGG CTACGCGC

18

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.6U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTCTTTGCCT CCTCAACCAT TG

22

## (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..22
  - (D) OTHER INFORMATION: /note= "JORAP2.6L"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCTGAGTTCC AACATTTTCG GG

22

## (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- ay
- (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..22
    - (D) OTHER INFORMATION: /note= "JORAP2.7U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAAATTGGTA ACTCCGGTTC CG

22

## (2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..22
  - (D) OTHER INFORMATION: /note= "JORAP2.7L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCATTTTGCT TTGGCGCATT AC

22

## (2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "JORAP2.8U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCGTTACGC CTCTACCGG

19

## (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "JORAP2.8L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCCGTCTTC CAGAACGTTC

20

## (2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "JORAP2.9U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ATCACGGATC TGGCTTGTT C

21

## (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "JORAP2.9L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCCTTCTTCC GTATCAACGT CG

22

## (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "JORAP2.10U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTCAACTCCG GCGGTTACG

19

## (2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "JORAP2.10L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TCTCCTTATA TACGCCGCCG A

21

## (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..23  
(D) OTHER INFORMATION: /note= "JORAP2.11U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAGAAGAGCA AAGGCAACAA GAC

23

## (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- ap*  
(A) NAME/KEY: -  
(B) LOCATION: 1..23  
(D) OTHER INFORMATION: /note= "JORAP2.11L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGTTGTTAGG AAAATGGTTT GCG

23

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..25  
(D) OTHER INFORMATION: /note= "JORAP2.12U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAACCATTCG TTTTCACTTC GACTC

25

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "JORAP2.12L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCACAGAGCG TTTCTGAGAA TTAGC

25

## (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "AP2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGTGGGATC TAAACGACGC AC

22

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "AP2L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCTTGGTC CACGCCGAC

19

## (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.1U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AAGAGGACCA TCTCTCAG

18

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.1L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AACACTCGCT AGCTTCTC

18

## (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.2U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGGTTCAGCA GCCAACAC

18



## (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..19
  - (D) OTHER INFORMATION: /note= "RAP2.2L primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CAATGCATAG AGCTTGAGG

19

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..18
  - (D) OTHER INFORMATION: /note= "RAP2.4U primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ACGGATTTCATCATCGGAG

18

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..19
  - (D) OTHER INFORMATION: /note= "RAP2.4L primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CTAAGCTAGA ATCGAATCC

19

## (2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.5U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TACCGGTTTC GCGCGTAG

18

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "RAP2.5L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CACCTTCGAA ATCAACGACC G

21

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "RAP2.6U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTCCCCGAAA ATGTTGGAAC TC

22

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "RAP2.6L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TGGGAGAGAA AAAATTGGTA GATCG

25

## (2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.7U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CGATGGAGAC GAAGACTC

18

## (2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.7L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTCGGAACCG GAGTTACC

18

## (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..19
  - (D) OTHER INFORMATION: /note= "RAP2.8U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TCACTCAAAG GCCGAGATC

19

## (2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- ap
- (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..19
    - (D) OTHER INFORMATION: /note= "RAP2.8L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TAACAACATC ACCGGCTCG

19

## (2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..18
  - (D) OTHER INFORMATION: /note= "RAP2.9U primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCTT AGGAGGAG

18

## (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.9L primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGCCTCATAT GAGTCAGAG

19

## (2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.10U primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCCCGGAGCT TTTAGCCG

18

## (2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "RAP2.10L primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAACCCGTTT CAACGATCC

19

## (2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "RAP2.11U primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TTCTTCACCA GAAGCAGAGC ATG

23

## (2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "RAP2.11L primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTCCATTCAT TGCATATAGG GACG

24

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "RAP2.12U primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GCTTTGGTTC AGAACTCGAA CATC

24

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "RAP2.12L primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AGGTTGATAA ACGAACGATG CG


22

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:


 Lys Lys Ser Arg  
 1

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "RAP2.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCATCGCCAC GATCAACC

18

## (2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -  
 (B) LOCATION: 1..18  
 (D) OTHER INFORMATION: /note= "RAP2.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AGCAGTCCAA TGCGACGG

18

## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

*ap* (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Trp Ala Ala Glu Ile Arg Asp  
1                    5

## (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Ala Asp Ser  
1

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